

Running head: Exposure assessment of *L. monocytogenes* in goat-cheese

Retrospective analysis of a *Listeria monocytogenes* contamination episode in raw milk goat cheese using quantitative microbial risk assessment tools

L. Delhalle ^{a*}, M. Ellouze ^b, M. Yde ^c, A. Clinquart ^a, G. Daube ^a and N. Korsak ^a

^a University of Liège, Faculty of Veterinary Medicine, Department of Food Science, Sart-Tilman, B43bis, 4000 Liege, Belgium

^b IFIP, French Institute for Pig and Pork Products, Fresh and Processed Meats Department, 7 Avenue du Général de Gaulle, 94 704 Maisons Alfort, France.

^c Scientific Institute of Public Health, Bacteriology section, Rue Juliette Wytsmanstraat 14, 1050 Brussels, Belgium.

*Corresponding author:

University of Liège, Faculty of Veterinary Medicine, Department of Food Science, Sart-Tilman, B43bis, 4000 Liege, Belgium

Tel: 32 4 366 40 40, fax: 32 4 366 40 44

Email address: l.delhalle@ulg.ac.be (L. Delhalle)

Keywords: Exposure assessment; goat-cheese; *L. monocytogenes*; sensitivity analysis; risk mitigation

Abstract

In 2005, the Belgian authorities reported a *Listeria monocytogenes* contamination episode in cheese made from raw goat's milk. The presence of an asymptomatic shedder goat in the herd caused this contamination. On the basis of data collected at the time of the episode, a retrospective study was performed using an exposure assessment model covering the production chain from the milking of goats up to delivery of cheese to the market. Predictive microbiology models were used to simulate the growth of *L. monocytogenes* during the cheese process in relation with temperature, pH and water activity. The model showed significant growth of *L. monocytogenes* during chilling and storage of the milk collected the day before the cheese production (median increase of 2.2 log CFU/ml) and during adjunction of starter and rennet to milk (median increase of 1.2 log CFU/ml). The *L. monocytogenes* concentration in the fresh unripened cheese was estimated to be 3.8 log CFU/g (median). This result is consistent with the number of *L. monocytogenes* in the fresh cheese (3.6 log CFU/g) reported during the cheese contamination episode. A variance-based method sensitivity analysis identified the most important factors impacting the cheese contamination, and a scenario analysis then evaluated several options for risk mitigation. Thus, by using Quantitative Microbial Risk Assessment (QMRA) tools, this study provides reliable information to identify and control critical steps in a local production chain of cheese made from raw goat's milk.

The safety of soft cheese made from raw milk is debated with regards to several micro-organisms of concern such as *Salmonella*, enterohemorrhagic *E. coli*, toxin-producing *Staphylococcus aureus* and *Listeria monocytogenes* (9). Cheese made from raw milk may be an important source of human listeriosis (16, 30, 31).

In 2005, a *Listeria monocytogenes* contamination episode in goat cheese made from raw milk was reported by the Belgian Federal Food Agency for the Safety of the Food Chain (FASFC).

Using the collected information, we have undertaken a retrospective study based on a quantitative microbial risk assessment (QMRA) method. QMRA is a scientifically based method for modelling the fate of pathogenic micro-organisms along the food chain and for assessing the associated risk of developing adverse effects for the consumer (27). Selected QMRA tools could be used to focus only on the food process and to provide options to reduce the level of contamination of the final product.

Field and laboratory collected data were used to implement the exposure assessment model from the milking of the goats up to the storage of end products in the farm. The final output is the *L. monocytogenes* contamination of goat cheese made from raw milk, due to the presence in the herd of an asymptomatic milk-shedder goat. The model was established in accordance with the *Codex Alimentarius* Commission guidelines (13). Dynamic predictive microbial models were used to follow the bacterial population during food processing by taking into account the temperature, pH and water activity (38). Sensitivity analysis was performed to identify the most important factors impacting *L. monocytogenes* concentration in the cheese (40). Finally, valuable options for risk mitigation were proposed and evaluated using scenario analysis.

MATERIALS AND METHODS

Description of the herd. The herd is composed of 350 goats from the “Alpine” breed. The farm is located in Wallonia (southern part of Belgium). The feed distributed to the goats is mainly composed of hay and grass silage with low moisture and made from herbage stored by the farmer himself. The goats’ milking yield is estimated to average 3.1 litres per goat per day (fat content and average total protein content of 3.1% and 3.4%, respectively).

The farmer and the veterinarian have suspected cases of listeriosis among the goats, especially in winters with extremely cold conditions or when molds were observed on hay or silages. The following symptoms were observed in the animals: nervous signs (e.g. ataxia), blindness or reduction of sight ability and spontaneous abortions. No analyses were performed on clinical specimens to confirm the diagnosis.

The cheese making process. The cheese production is based on several steps as shown in Figure 1. Tables 1 and 2 describe the inputs and the calculations used in the model. The first step is to refrigerate and cool the evening milk production from 39.5°C to 10°C during 14h. During this step, the growth of *L. monocytogenes* is possible, and the step was simulated attempting to replicate the temperature evolution, pH (6.63) and water activity (1) of the milk.

As a second step, the milk of the morning is collected at 39.5°C, and stored during 1h. *L. monocytogenes* growth is also possible during this second step. The evening production is then mixed with the morning production and the raw milk mixture is allowed to settle during 1h at room temperature in order to achieve an internal temperature of 21-22 °C. A commercial starter culture (PAL Bioprotect D and Pal LC Mix 6, Standa, Caen, France) is added to the raw milk without heating. The starter is received by the processor in the form of a powder that is reconstituted by mixing 200 g in 1 litre of milk to form the “stock solution”. Milk is seeded by adding 20 ml of the “stock solution” to 100 litres of raw milk and is then kept at 22°C for a duration of 2h in order to start the fermentation process. In the fifth step, commercial rennet

(préasure simple Berthelot®, laboratories Abia, Meursault, France) is added to the fermented milk (15 ml/100 litres raw milk). The mixture is then allowed to settle at 22°C for an additional period of 22h. The next step consists of draining off the water by ladling the fresh cheese (the curds) into plastic molds at 22°C. Molds are turned over three hours later. After 0,5h, the cheeses are separated from the molds, placed on metallic racks and stored in a dryer room with an air temperature of between 14.5 and 18°C and relative humidity of 70 to 75%. The seventh step is salting. This operation is repeated twice. Cheeses are first manually turned over and hand-salted on their external surfaces at a temperature of 20°C during 24h. They are replaced back in the dry room, after which they are salted on the other side during 48h at 16°C. The final products are cooled during 48h in the chilling room (with a relative humidity of close to 100%) at 1°C until distribution.

The main cheese production on this farm is of unripened fresh cheese, but other productions are sometimes performed. For non-fresh cheese, the previous diagram is completed by a ripening step that may last 6 to 7 days, during which cheeses are turned over daily. Some cheeses are dried off in an automatic apportioner or distributor. The drying off may also take place in cellulose bags or in a cheese strainer. The cheeses' final presentations may also vary.

The number of portions of 100g-cheeses produced in a week is estimated to be 5,000 cheeses in average, from which 95 % are fresh (not ripened). Around five liters are necessary to produce 1 kg of fresh cheese (due to the loss of whey during the process).

Technological analysis performed by the farmer. The farmer uses the Dornic Acidity as a quality indicator during the production process. One Dornic acid degree (°D) is equivalent to 1 mg of lactic acid in 10 ml of milk or 0.1 g/L (23). This test is performed on the milk before fermentation to gain a rough assessment of its hygienic quality and on the curds to monitor the decrease in pH.

Microbiological analysis. Once the contamination episode was identified by the FASFC, several microbiological investigations were conducted. An external accredited laboratory performed these analyses. *L. monocytogenes* was detected on milk and cheese samples using the horizontal method NF EN ISO 11290-1 (3). The method NF EN ISO 11290-2 was used to quantify *L. monocytogenes* in the samples (4).

Technological analysis. To characterize changing factors during the cheese making process, several technological parameters were measured at different stages done at the time of the outbreak by the accredited laboratory. These parameters were:

- pH: Laboratory method derived from the ISO 2917:1999 (2), using a Knick 765 Laboratory pH meter (Escolab, Kruibeke, Belgium).
- Water-activity (a_w): method based on the ISO 21807:2005 (5) using a Novasina TH200 water activity meter (Lachen, Switzerland).
- Salt content: Laboratory own method adapted the ISO 1841-1:1996 (1).

Further characterization of isolates. After identification of the species, the Belgian national reference lab serotyped the isolates ((Institute of Public Health (IPH), Brussels, Belgium) according to a standard protocol using a commercial agglutination test (Denka Seiken, Tokyo, Japan) based on antibodies specifically reacting with somatic (O) and flagellar (H) antigens (46).

Susceptibility of the strains to ten antibiotics was determined (Etest, AB BIODISK). Susceptibility to arsenic and cadmium was also performed by the method described in the literature (33).

Pulsed-Field Gel Electrophoresis (PFGE) was applied in accordance with the US PulseNet protocol describing PFGE after DNA digestion with the enzymes *ApaI* and *AscI*. PFGE enables the cutting of genomic DNA into a number of fragments comprised between 10 and 20, that facilitates the computer analysis. The regular change of the current direction in the gel

allows the migration of DNA fragments (26). Analysis of banding patterns was performed with an ImageMaster video documentation system (Amersham Pharmacia Biotech) and Fingerprinting II Informatix software (Bio-Rad).

QMRA applied to *L. monocytogenes* in raw goat's milk cheese – hazard identification. In this study, the hazard is *L. monocytogenes* and the final output of the exposure assessment model is the level of contamination of raw goat's milk cheese. *L. monocytogenes* is ubiquitous and is described as a short rod, catalase-negative, Gram positive micro-organism with a special motility at 25°C (29). In animals this bacterium has been observed since 1926 and has been recognized as a major food borne pathogen since the 1980s. It is an intracellular pathogen that can cause a sometimes fatal human disease named “listeriosis”, especially prevalent among high-risk populations, namely the elderly (>60) and immuno-compromised patients. In particular, *L. monocytogenes* can cause spontaneous abortion in pregnant women as well as meningitis and septicaemia in newborn infants and immuno-compromised people. The case-fatality risk can reach 34% (9).

According to the report of the European Food Safety Authority (EFSA), the number of reported cases of confirmed human listeriosis was estimated to be 1,381 in 2008 (21). De Buyser et al. (16) have reviewed the relationship between food borne diseases outbreaks and milk products in France for the period from 1988 to 1997. This study showed that, when the food vehicle was precisely known, milk products accounted for 6% of the outbreaks caused by food borne pathogens.

In 1995 “Brie de Meaux” cheese was identified as the source of 36 listeriosis human cases (including 11 deaths), while in 1997 Livarot Pont-L'évêque cheese was implicated in 14 cases (16, 30).

In Belgium, many cases of listeriosis are not reported in the official statistics since most cases of human listeriosis cause mild to moderate self-limited disease, and the patient does

not automatically consult a physician. Moreover, it remains difficult to assess the number of human listeriosis caused specifically by the ingestion of contaminated cheese made from raw goat's milk. Vanholme et al. (47) reported that the number of cases of listeriosis officially reported in Belgium in 2005 was 40, but different food sources were involved including beef, pork, dairy products, fish and ready-to-eat products (RTE). It was therefore not possible to estimate the number of listeriosis clearly attributable to cheese made from raw goat's milk. However, a serotyping comparison was possible. In 2005 serotypes 1/2a caused 55 % of cases of listeriosis reported in Belgium and serotype 4b caused 42.5% (47).

QMRA applied to *L. monocytogenes* in raw goat's milk cheese – exposure assessment.

Fresh unripened cheese was chosen for the exposure assessment model because it is the most sold product. Furthermore, data for this product are available to support a retrospective investigation. The principles of the Modular Process Risk Model (MPRM) methodology were used to break down the food production chain into modules (36) and to follow the bacteriological concentration of the pathogen throughout the process, including the eight modules presented in Figure 1: (1) storage of the evening milk, (2) storage of the morning milk, (3) mixing of the morning and evening milk, (4) adjunction of the starter to the milk, (5) adjunction of rennet to the milk, (6) draining off of curds, (7) salting at ambient temperature and (8) cooled storage. Each module generates an output that is used as an input for the next module. The simulated events are identified for each module: growth, mixing and/or partitioning. Input values are classified as process inputs, microbiological or food characteristics. Table 1 describes parameters as fixed values or probability distributions reflecting the natural variability.

Growth was simulated using primary and secondary predictive microbiology models.

A three phase linear model without lag was used to simulate the growth of *L. monocytogenes* as a function of time (11) as shown in Equation 1.

$$\begin{aligned}\ln(N_{t_k}) &= \ln(N_{t_{k-1}}) + \mu_{\max_{i(k)}} \Delta t_k, \text{ if } N_{t_k} < N_{\max} \\ &= \ln(N_{\max}), \text{ if } N_{t_k} \geq N_{\max}\end{aligned}$$

Equation 1

where i is one of the eight modules of the process with $i = 1$ to 8

k is the recorded parameter index in the stage i with $k = 1, \dots, n$

Δt_k is the time interval with $\Delta t_k = 1$ hour

N_{t_k} is the bacterial population at time t_k (CFU.ml-1 or CFU.g-1)

N_{\max} is the maximal bacterial population (CFU.ml-1 or CFU.g-1)

The effects of temperature, pH and water activity on the maximum growth rate μ_{\max} of

L. monocytogenes were modelled by a multiplicative function with interaction (Equation 2)

derived from the cardinal model (Equation 3 and 4) (8, 14):

$$\mu_{\max_{i(k)}} = \mu_{opt} CM_2(T_{i(k)}) CM_1(pH_{i(k)}) CM_1(a_{wi(k)}) \xi(T_{i(k)}, pH_{i(k)}, a_{wi(k)})$$

Equation 2

$$CM_n(X) = \begin{cases} 0, & X \leq X_{\min} \\ \frac{(X - X_{\max})(X - X_{\min})^n}{(X_{opt} - X_{\min})^{n-1} [(X_{opt} - X_{\min})(X - X_{opt}) - (X_{opt} - X_{\max})((n-1)X_{opt} + X_{\min})]}, & X_{\min} < X < X_{\max} \\ 0, & X \geq X_{\max} \end{cases}$$

Equation 3

$$\xi(\varphi(T, pH, a_w)) = \begin{cases} 1, \psi \leq \theta \\ 2(1-\psi), \theta < \psi < 1 \\ 0, \psi \geq 1 \end{cases} \quad \text{with} \quad \psi = \sum_i \frac{\omega(X_i)}{2 \cdot \prod_{j \neq i} (1 - \omega(x_j))},$$

$$\omega(X) = \left(\frac{X_{opt} - X}{X_{opt} - X_{\min}} \right)^3 \quad \text{and} \quad \theta = 0.5.$$

Equation 4

where $\mu_{\max_{i(k)}}$ is the bacterial growth rate following the environmental factors at time t_k

$T_{i(k)}$ is the recorded temperature at time t_k (°C)

$pH_{i(k)}$ is the recorded pH at time t_k

$a_{wi(k)}$ is the recorded water activity at time t_k

X_{min} , X_{opt} and X_{max} , are the minimal, optimal and maximal temperature, pH and water activity of growth for *L. monocytogenes*.

Table 2 gives the calculation details to assess the final number of *L. monocytogenes* in a typical serving of fresh goat cheese.

The starting point of the model is the initial concentration of *L. monocytogenes* in the milk from the right part of the mammary gland of the contaminated goat ($4.3 \cdot 10^2$ CFU/ml or 2.63 log CFU/ml ; source: FASFC). This concentration is used in the first module to calculate the *L. monocytogenes* number per milking and to deduce the concentration of *L. monocytogenes* in the tank before the overnight storage of the evening milking. It is assumed that this concentration is a Poisson distribution and that the milk temperature decreases linearly overnight between the beginning and the end of the cooling. There is no heat exchanger plate in the food process. The temperature of the evening milk decreases slowly in the tank overnight. Predictive microbiology models simulate the growth of *L. monocytogenes* during this storage period.

The second module is dedicated to the storage of the morning milking, where the *L. monocytogenes* concentration in the tank before the storage of the morning milk is assessed and implemented in predictive microbiology models to simulate the pathogen evolution in the tank after the morning storage. The initial temperature of this second module corresponds to the temperature at the end of the milking, 39.5°C, while the final temperature obtained after one hour storage is sampled among a Pert distribution, with a most likely final temperature of 22°C and minimum and maximum final temperatures of 20 and 24°C, respectively. It is explained by the mixing of the evening and the morning milk in the same tank at the end of the storage of the morning milk.

In the third module, the concentration of the pathogen in the tank after mixing is deduced from the concentrations of *L. monocytogenes* in the tank before and after storage to

be implemented in modules 4 and 5 representing the steps of starter and rennet adjunction to milk. Using predictive microbiology models (equations 1 to 4), the *L. monocytogenes* concentration in milk before draining off the curdles is calculated. It is assumed that the distribution of the pathogen is heterogeneous during the curdling of milk. Following Bemrah et al. (9), the *Listeria* cells concentrates at a level of 90 % in the curds and 10 % in the whey. The start and end temperatures of this step are sampled among a Pert distribution, with a most likely value of 22°C and minimum and maximum values of 20 and 24°C, respectively. The pH is considered to decrease linearly between the start and the end of the fermentation process according to equation 5.

$$pH = -0.1005t + pH_i \quad \text{Equation 5}$$

This linear relation is based on the evolution of pH and Dornic acidity with time in the fermented milk (data not shown). A correlation was made between the values of Dornic acidity measured by the farmer and the pH measurements in the laboratory.

The concentration in milk before draining off the curdles is used in module 6 to assess the amount of pathogen per cheese before storage and salting. Finally, in modules 7 and 8, predictive microbiology models are used to characterize the number of *L. monocytogenes* per serving of cheese, taking into account the effects of temperature, pH and a_w as shown in Figure 1.

Technological parameters measured in the milk and at different stages of ripening of the final product (2 measurements per sample) are used according to Table 1 and 2.

The model was developed using @Risk 4.5.5 (Palisade, Ithaca, N.Y.), an add-in for Microsoft Excel. Input values of each module were implemented as estimated distributions of probability, to describe the natural variability associated with input factors. We used 50,000 iterations with the latin hypercube sampling (LHS) method to obtain stochastic estimates of the output variables (32). Finally, the estimated median concentration of *L. monocytogenes* in

a serving of cheese was compared with the concentration measured in the fresh cheese by the FASFC.

QMRA applied to *L. monocytogenes* in raw goat's milk cheese – sensitivity analysis. In order to identify the subset of the most important factors of the exposure assessment model, a global sensitivity analysis (SA) was performed using the Saltelli method (40). This is a numerical based procedure for computing first order indices, S_i , and total effect indices, St_i , for all the factors i ($i=1,\dots,k$) of the studied model. Each first order index S_i provides an estimate of the relative importance of the factor X_i taken singularly, while the total effect index St_i reflects the cooperative effects of the factor X_i and its non linear interactions with the other factors (40, 41). The method is fully described in the literature (40-44). Its implementation for microbial growth models is provided in Ellouze et al. (20), and recently this method was applied to a QMRA of *L. monocytogenes* in deli meats (12).

To calculate these indices, a characterization of the range of variation of the several factors of the model is necessary. These factors are presented in Table 3 and are composed of two categories of factors. The first category includes factors related to the milk production such as the number of goats and the quantity of milk per milking. The second category includes factors representing the characteristics of the pathogen such as its cardinal values, its optimum growth rates in milk and cheese, etc.

A total set of 35 input factors was thus identified for the exposure assessment model. Their ranges of variation were obtained directly from experimental data provided by the farmer (minimum and maximum observed values) or from the 1st and 99th percentiles of the distributions characterizing their variability.

Once the ranges of variation of the different input factors were characterized, their indices were computed according to the following procedure. Two matrices A and B of N lines corresponding to the N simulation runs ($N=5.10^4$) and k columns corresponding to the k

studied factors ($k=35$) were generated using the LHS method as a space filling design. The matrices A and B were filled with respect to the range of variation of each factor (Table 3) and the model was run on each row of the two matrices to provide the response vectors Y_A and Y_B . Then, k matrices C_i , $i=1, \dots, k$, were generated, containing all the columns of matrix B except the i^{th} column which was replaced by the i^{th} column of matrix A , and the global model was run again to provide the vectors Y_{C_i} . Finally, the first order indices, S_i , and total effect indices, St_i , were calculated according to the following formula (40):

$$S_i = \frac{\frac{1}{N} \sum_{u=1}^N Y_A^{(u)} Y_{C_i}^{(u)} - g_0}{\frac{1}{N} \sum_{u=1}^N Y_A^{(u)} Y_A^{(u)} - f_0^2}$$

$$St_i = 1 - \frac{\frac{1}{N} \sum_{u=1}^N Y_B^{(u)} Y_{C_i}^{(u)} - f_0^2}{\frac{1}{N} \sum_{u=1}^N Y_A^{(u)} Y_A^{(u)} - f_0^2} \quad \text{Equation 6}$$

$$\text{with} \quad f_0 = \frac{1}{N} \sum_{u=1}^N Y_A^{(u)}$$

$$g_0 = \frac{1}{N} \sum_{u=1}^N Y_A^{(u)} Y_B^{(u)}$$

The bootstrap method (18) was used to assess the confidence intervals of these indices through reliable estimates without additional computational effort (6). Values obtained for the response vectors were sampled with replacement for 10^4 bootstrap replicates, and, for each replicate, the indices S_i and St_i were calculated, leading to a bootstrap estimate of the distribution of the sensitivity indices. The 95% confidence intervals of the indices were thus defined using the 5th and 95th percentiles and were used to identify the most important factors as those for which the total effect indices were significantly different from 0.

QMRA applied to *L. monocytogenes* in raw goat's milk cheese – Scenario analysis.

The effect of some variables in the exposure assessment model was assessed using simulation scenarios to provide valuable information on possible ways of reducing the concentration of

pathogens in a final serving (17, 48). This assessment was achieved by selecting various combinations of input variables.

This procedure is commonly known as a “what if scenario” (49). In the present study, a first run of the model without modifications was performed to provide the baseline results of the selected outputs. Three scenarios were tested in order to look for ways of reducing the risk, and one worst-case scenario was tested to assess the magnitude of the risk increase in such a case:

- Scenario 1: Install a heat exchanger plate to obtain a temperature of 7 °C directly after milking and maintain a constant temperature during the overnight storage.
- Scenario 2: Reduce pH by 0.5 units at the start of adjunction of ferment and rennet. This could be achieved, for example, by adjunction of a common food acid such as lactic acid or glucono delta lactone.
- Scenario 3: Increase efforts during production by combining Scenarios 1 and 2.
- Scenario 4: Two shedder goats in the herd each excreting the same amount of *L. monocytogenes* as the goat on the farm studied.

Decontamination treatments, such as pasteurization, are not considered to respect the initial characteristics of the product. The results are displayed as the concentration of *L. monocytogenes* in a cheese serving.

RESULTS

Alert investigations. Table 4 summarizes the information in relation to the anamnesis of the case.

The serotyping results of the first external laboratory showed that the strain isolated from the cheese belongs to serotype 1/2a with a characteristic β -hemolysis. Three days later another external laboratory analyzed the pools of milk collected from the goats. One positive pool

(milk collected from twenty goats) was detected, and from the sources of that milk one clearly positive goat was identified in the herd.

The goat was transferred to the Faculty of Veterinary medicine. The results of milk samples were as follows:

- 2.6 log *L. monocytogenes* /ml in the milk collected from the right part of the mammary gland
- absence of *L. monocytogenes* in 25 g of the milk collected from the left part of the mammary gland

Enumerations were also made on the cheeses with the following results:

- concentration of *L. monocytogenes* in fresh not ripened goat cheese: 3.6 log CFU/g
- concentration of *L. monocytogenes* in ripened goat cheese: 3.8 log CFU/g
- concentration of *L. monocytogenes* in ripened goat cheese coated with charcoal: 3.7 log CFU/g

The *L. monocytogenes* isolates collected from the milk and cheese were sensitive to the 10 investigated antibiotics and were sensitive to arsenic and cadmium.

The pulsotyping results showed that isolates from the milk of the isolated goat and from the contaminated cheese belonged to the same pulsovar A (data not shown). In 2005, the Belgian *Listeria* reference laboratory received 40 strains of *L. monocytogenes* of human clinical origin: 16 strains were of serovar 1/2a, of which 7 strains were arsenic and cadmium sensitive. However, pulsotyping excluded genetic matching for these 7 strains with the cheese and milk isolates from the goat farm (data not shown). This means that no cases of human listeriosis could be traced back to the consumption of the contaminated goat cheese.

QMRA model – baseline results. Table 5 gives the base line results of the exposure assessment and the risk characterization modules. Since these models were built to take into account the natural variability associated with the different input factors, the results are

expressed as distributions. The median estimates (50th percentile) associated with the 5th and 95th percentiles presented in Table 5 give a good assessment of the results. *L. monocytogenes* concentrations results are converted to a logarithmic scale (base 10).

The modular exposure assessment model shows a significant growth of *L. monocytogenes* during chilling and storage of the milk collected the day before the cheese production (an increase of 2.2 log CFU/ml for the median). Figure 2a gives the pathogen evolution at this step with dynamic temperature conditions. During the storage of the evening milking overnight, the milk is slowly chilled from 39.5°C to 10°C. The growth rate of *L. monocytogenes* is directly related to the temperature, which explains the observed brake of microbial growth during the chilling process.

A less important increase (1.2 log CFU/ml for the median) was obtained after the starter and rennet adjunction to milk. This result is explained by the pH drop in the milk due to the fermentation activity, which gradually decreased the pH down to 4.41. Figure 2b shows the evolution of *L. monocytogenes* after the adjunction of ferment and rennet. At the end of the fermentation, the pH value was close to the minimum pH for *L. monocytogenes* growth ($pH_{min}=4.19$), which can explain the limited growth of the pathogen after the fermentation.

The estimated median *L. monocytogenes* concentration in a serving of cheese (Table 5) was equal to 3.8 log CFU/g. This estimate was in compliance with the concentration of *L. monocytogenes* reported in the fresh cheese by the FASFC during the contamination episode, which was equal to 3.6 log CFU/g. The model gives satisfactory results by comparison with the data provide by the FASC.

Sensitivity analysis. The global sensitivity analysis results are depicted in Table 6, which presents the first order and total effect indices of each factor with their confidence bootstrap intervals.

Total effect indices and first order indices are especially powerful when performing SA in cases of non additive and non linear models (6) such as the exposure assessment part of the model used in this study. In fact, as can be deduced from Table 6, the sum of the non negative first order indices (S_i), which account for the individual contribution of each factor into the variance of the output, is less than 1, which means that the variance of the output cannot be explained solely by the sum of the individual effects of each factor, but is also attributed to the effects of interactions.

This is also confirmed by the relatively substantial difference observed between the St_i and the S_i for all the important factors, which indicates the significant role of interactions. Ranking the 35 factors of the model according to their total effect indices identified the most important factors. Total effect indices were chosen as ranking criteria because they indicate the effect of each studied factor and its interactions with the other factors. They were therefore preferred to the first order indices, which only reflect the relative importance of the factor taken singularly.

The confidence intervals associated with the total effect indices were examined, and the factors with confidence intervals significantly different from 0 were identified as the most important factors. Four factors were thus selected: the duration of the first salting step ($D_{salting1}$), the minimum pH for *L. monocytogenes* growth pH_{min} , the optimal growth rate of *L. monocytogenes* in milk (μ_{opt_milk}) and the initial *L. monocytogenes* concentration (N_0).

Scenario analysis. The results of the scenario analysis are displayed in Table 7. The outputs are the amount of *L. monocytogenes* per cheese serving. The results obtained for the first scenario show a reduction of 1.5 log CFU/g compared with the baseline results and could be a good alternative for risk mitigation. The results obtained for the second scenario prove that a reduction of 0.5 pH units could only reduce by 0.2 log CFU/g the median concentration compared with the baseline results. The results obtained for the third scenario, which

combines Scenarios 1 and 2, show a reduction of 1.8 log CFU/g of the median concentration compared with the baseline results. The last scenario shows a significant increase of 0.4 log *L. monocytogenes*/g in a cheese serving compared with the baseline results.

DISCUSSION

Few QMRA concerning cheese contaminated with *L. monocytogenes* have been published (9, 22). This is probably due to the difficulty of obtaining valuable data to develop a complete QMRA of the cheese production chain. In fact, a frequently heard criticism of QMRA is that it is extremely data hungry (27), and its final results depend heavily on the quality of the input data, particularly when variability and uncertainty are taken into account.

In an attempt to simulate the entire production chain of cheese made from raw goat's milk, an exposure assessment that takes into account different sources of natural variability was developed in this study. The results showed a significant growth of *L. monocytogenes* during the cheese manufacturing process, especially after the evening milk storage (median increase of 2.2 log CFU/ml) and during the steps of starter and rennet adjunction to milk (median increase of 1.2 log CFU/ml).

However, it is thought that the acidification process experienced during cheese making is not favourable to pathogen growth. In fact, Schwartzman et al. (45) have shown that there was no growth of *L. monocytogenes* 4b isolated from cow faeces during the process of cheese making from raw cow's milk, but growth was observed on the same process when pasteurized milk was used, which is probably due to the absence of a competitive flora. Some studies have already reported the importance of the presence and/or the level of the competitive flora on the growth/no growth of *L. monocytogenes* in several foods (25, 34). The model developed in this study did not specifically include the effect of the competitive flora, but the simulated median result for the *L. monocytogenes* concentration in the fresh cheese was equal to 3.8 log CFU/g which was consistent with the concentration of *L. monocytogenes* (3.6 log CFU/g)

detected by the FASFC in the contaminated fresh cheese. This result does not constitute a validation, it means only that the model seems to have a good behaviour with the collected data.

Due to the lack of data, this exposure assessment model like any other may suffer descriptive errors that represent incorrect or insufficient information (24). In fact, the lack of data sometimes made it necessary to build in several assumptions. First, the storage temperature of the evening milking was considered to decrease linearly during the night. Some authors have attempted to model the temperature evolution during the cheese making process (28), but as the linear decrease in temperature gave satisfactory simulated temperatures compared to the observed temperatures, this assumption was adopted to avoid over-parameterization of the exposure assessment model. Second, the excretion of *L. monocytogenes* by the contaminated shedder goat was considered to be the same for each production day. Third, *L. monocytogenes* distribution was supposed to be heterogeneous during the curdling of milk with a level of 90 % in the curds and 10 % in the whey. This last assumption was based on the study of Bemrah et al. (9).

In spite of these limitations, this study attempts to simulate the contamination flow of raw goat cheese produced on a local dairy farm and to relate the final concentration of *L. monocytogenes* in cheese with observed epidemiological and microbiological data made in a contamination alert episode in 2005.

This study also suggests risk mitigation scenarios to reduce the concentration of *L. monocytogenes* at the end of the cheese process. The first scenario considered a faster chilling of the milk from the initial temperature of 39.5 °C down to 7 °C. At this temperature, the growth rate of *L. monocytogenes* is considerably reduced during the storage of the milk over night, resulting in a reduction of 1.5 log CFU/g in the final concentration of the pathogen in the cheese. The second scenario evaluated a pH reduction of 0.5 units at the start of the

adjunction of ferment and rennet. This intervention could be simply achieved by lactic acid adjunction, for example, and could reduce the median growth of *L. monocytogenes* by 0.2 log CFU/g. The third scenario, which is a combination of the previous two, showed a reduction of 1.8 log CFU/g of the median *L. monocytogenes* concentration compared with the model baseline results. The last scenario, involving two shedder goats in the herd, showed a significant increase of 0.4 log *L. monocytogenes* concentration in a serving cheese compared with the base line results.

The results of the sensitivity analysis gave complementary information and identified four factors significant for their impact on the concentration of *L. monocytogenes* in cheese. Among the four significant factors, pH_{\min} and μ_{opt_milk} are characteristics of the pathogen for which it is therefore impossible to control. However, the sensitivity analysis also uncovered the potential to act on technological parameters, such as the salting time to reduce the number of contaminated cheeses. It is also feasible to perform effective actions to reduce the initial contamination level N_0 . Efficient and frequent monitoring of the pathogen in the food chain could significantly reduce its concentration in the end product and could be easily achieved by means of a more stringent sampling plan for the raw milk and cheese.

In the future it would be interesting to identify sources of *L. monocytogenes* contamination. A few studies have explored sources of contamination on farms. Danielsson-Tham et al. (15) studied an outbreak of gastro-intestinal listeriosis affecting 120 humans in Sweden after consumption of raw-milk cheese produced in a summer farm composed of dairy cattle and goats. The authors traced back the origin of contamination in the cheese by investigating the different sources in the summer farm and in the cheese production facilities. The most likely hypothesis, although not strictly confirmed, was the presence of a goat in the herd with a subclinical mastitis which led to the contamination of equipment in the cheese production facilities, specifically a wooden bench and the home-made brine. Nightingale et al.

(37) explain that the patterns of contamination on farms are not very clear: is the feed the main source of infection in animals and hence in the milk products or is the animal itself? Grazing seems not to be the predominant route of infection, but poorly made silages (e.g. corn silages with a high end-pH value) may lead to an amplification of the levels of *Listeria* species in animals. Comparing the prevalence of *Listeria monocytogenes* on case farms (farms with a history of animal listeriosis) and on control farms (farms with no reports of animal listeriosis) they observed that for small ruminants the prevalence was higher on case-farms. Yet, for cattle the prevalence was statistically equivalent between case and control farms.

Faecal contamination of the animals may explain the greater prevalence of listeriosis in small ruminants on case farms. If it is the cause, then faecal contamination may also increase the likelihood of *Listeria monocytogenes* contamination of raw milk. The fact that patterns of contamination appear quite different between the cattle and the goat populations led Danielsson-Tham et al. (15) to conclude that some ribotypes may be able to persist in the environment and others not. Wiedmann et al. (51) also concluded that multiple ribotypes may exist on a farm at the same time, colonizing differently depending on environmental factors, because the researchers observed in only one case a relationship between the strains isolated in clinical samples of animals and strains isolated from silages. In our study, we assume that the contamination of raw milk occurred mainly through the milk, even though *Listeria monocytogenes* could have been recovered from the faecal matter of the asymptomatic shedder goat.

Meyer-Broseta et al. (35), using different sampling strategies, noticed that *Listeria monocytogenes* occurs at a very low level in the tank. When the bulk tanker in the milk processing industry was contaminated (collecting different deliveries from cattle farms), the average prevalence for positive farms was 7.7% with contamination levels for

L. monocytogenes below 3 CFU/ml and a median of between $5 \cdot 10^{-2}$ and $1 \cdot 10^{-1}$ CFU/ml. Several authors have noticed that it is important to have a final pH-value in the silages that is lower than 5 in order to decrease the risk of listeriosis in ruminants (50, 51). In our case, the farmer observed a significant decrease of listeriosis cases in the goats after he had adapted his machine for producing hay and low-moisture grass-silages. He began cutting the grass higher, which may have reduced the contamination of the hay and silages by dirt and dust from the soil. This decrease in contamination may explain the decrease in observed cases of listeriosis in the goats. The farmer also observed that the remaining cases of listeriosis were more frequent during the winter season, which is consistent with findings in the scientific literature (10).

In conclusion, this retrospective study aims to simulate the fate of *L. monocytogenes* throughout a raw goat's milk cheese making process from milking to delivery to the market, using quantitative microbial risk assessment methodology. The results were satisfactory when compared with the epidemiological and microbiological observations of the alert investigations. The most important factors of the *L. monocytogenes* contamination were identified, and risk mitigation scenarios were evaluated to identify the most efficient strategies to reduce the risk of listeriosis in respect of the food characteristics.

Due to the lack of data for some parameters, the exposure assessment was based on several assumptions. Although continued work is needed to better evaluate risks to consumers, this study clearly demonstrated that QMRA tools and predictive modelling can be useful to increase food safety and should be gradually implemented in the coming years.

References

- 535
- 536
- 537 **1. Anonymous. 1996. ISO 1841-1 Viande et produits à base de viande -**
- 538 **Détermination de la teneur en chlorures. Partie 1 : méthode de Volhard. p. 1-4. *In* ISO**
- 539 **(International Organization for Standardisation), Genève (in French).**

- 540 **2. Anonymous. 1999. ISO 2917:1999(F) Viande et produits à base de viande -**
- 541 **mesurage du pH - méthode de référence p. 1-6. *In* ISO (International Organization for**
- 542 **Satndardization), Genève (In French).**

- 543 **3. Anonymous. 2004. NF EN ISO 11290-1 Méthode horizontale pour la recherche et**
- 544 **le dénombrement de *Listeria monocytogenes*. Partie 1 : Méthode de recherche -**
- 545 **Amendement 1 : modification des milieux d'isolement, de la recherche de l'hémolyse et**
- 546 **introduction de données de fidélité. Horizontal method for the detection and**
- 547 **enumeration of *Listeria monocytogenes*. Part 1 : Detection method - amendment 1:**
- 548 **modification of the isolation media, of the haemolysis test and inclusion of precision**
- 549 **data. p. 1-14. *In* CEN (European Committee for Standardisation), Bruxelles (in**
- 550 **French).**

- 551 **4. Anonymous. 2004. NF EN ISO 11290-2 Méthode horizontale pour la recherche et**
- 552 **le dénombrement de *Listeria monocytogenes*. Partie 2 : Méthode de dénombrement.**
- 553 **Amendement 1 : Modification du milieu d'isolement. Horizontal method for the**
- 554 **detection and enumeration of *Listeria monocytogenes*. Part 2: Enumeration method.**
- 555 **Amendment 1: modification of the enumeration medium. p. 1-4. *In* CEN (European**
- 556 **Committee for Standardisation), Bruxelles (in French).**

- 557 5. Anonymous. 2005. NF ISO 21807 Microbiologie des aliments - Détermination de
558 l'activité de l'eau. p. 1-8. In ISO (International Organization for Standardization)
559 Genève (in French).
- 560 6. Archer, G. E. B., A. Saltelli, and I. M. Sobol. 1997. Sensitivity measures,
561 ANOVA-like techniques and the use of bootstrap. *J. Statist. Comput. Simul.* 58:99–120.
- 562 7. Augustin, J. C. 1999. Modélisation de la dynamique de croissance des populations
563 de *Listeria monocytogenes* dans les aliments. p. 157. In, vol. PHD. Université de Lyon,
564 Lyon.
- 565 8. Augustin, J. C., V. Zuliani, M. Cornu, and L. Guillier. 2005. Growth rate and
566 growth probability of *Listeria monocytogenes* in dairy, meat and seafood products in
567 suboptimal conditions. *J. Appl. Microbiol.* 99:1019-42.
- 568 9. Bemrah, N., M. Sanaa, M. H. Cassin, M. W. Griffiths, and O. Cerf. 1998.
569 Quantitative risk assessment of human listeriosis from consumption of soft cheese made
570 from raw milk. *Prev Vet Med.* 37:129-45.
- 571 10. Brugère-Picoux, J. 2008. Ovine listeriosis. *Small Ruminant Res.* 76:12-20.
- 572 11. Buchanan, R. L., R. C. Whiting, and W. C. Damert. 1997. When is simple good
573 enough: a comparison of the Gompertz, Baranyi, and three-phase linear models for
574 fitting bacterial growth curves. *Food Microbiol.* 14:313-326.

- 575 12. Busschaert, P., A. H. Geeraerd, M. Uyttendaele, and J. F. Van Impe. 2011.
576 Sensitivity Analysis of a Two-Dimensional Quantitative Microbiological Risk
577 Assessment: Keeping Variability and Uncertainty Separated. *Risk Anal.* 31:1295-1307.
- 578 13. Codex Alimentarius Commission. 1999. Principles and guidelines for the conduct
579 of microbiological risk assessment. Codex Alimentarius Commission, Roma.
- 580 14. Couvert, O., A. Pinon, H. Bergis, F. Bourdichon, F. Carlin, M. Cornu, C. Denis,
581 N. Gnanou Besse, L. Guillier, E. Jamet, E. Mettler, V. Stahl, D. Thuault, V. Zuliani, and
582 J.-C. Augustin. 2010. Validation of a stochastic modelling approach for *Listeria*
583 *monocytogenes* growth in refrigerated foods. *Int. J. Food Microbiol.* 144:236-242.
- 584 15. Danielsson-Tham, M. L., E. Eriksson, S. Helmersson, M. Leffler, L. Ludtke, M.
585 Steen, S. Sorgjerd, and W. Tham. 2004. Causes behind a human cheese-borne outbreak
586 of gastrointestinal listeriosis. *Foodborne Pathog. Dis.* 1:153-159.
- 587 16. De Buyser, M. L., B. Dufour, M. Maire, and V. Lafarge. 2001. Implication of milk
588 and milk products in food-borne diseases in France and in different industrialised
589 countries. *Int. J. Food Microbiol.* 67:1-17.
- 590 17. Delhalle, L., C. Saegerman, W. Messens, F. Farnir, N. Korsak, Y. Van der Stede,
591 and G. Daube. 2009. Assessing interventions by quantitative risk assessments tools to
592 reduce the risk of human salmonellosis from fresh minced pork meat in Belgium. *J.*
593 *Food Prot.* 72:2252-2263.

- 594 18. Efron, B., and R. J. Tibshirani. 1993. An introduction to the bootstrap. Chapman
595 & Hall, New York.
- 596 19. Ellouze, M., and J. C. Augustin. 2010. Applicability of biological time
597 temperature integrators as quality and safety indicators for meat products. *Int. J. Food*
598 *Microbiol.* 138:119-129.
- 599 20. Ellouze, M., J. P. Gauchi, and J. C. Augustin. 2011. Use of global sensitivity
600 analysis in quantitative microbial risk assessment: Application to the evaluation of a
601 biological time temperature integrator as a quality and safety indicator for cold smoked
602 salmon. *Food Microbiol.* 28:755-769.
- 603 21. European Food Safety Authority. 2010. The Community Summary Report on
604 Trends and Sources of Zoonoses, Zoonotic Agents, Antimicrobial Resistance and
605 Foodborne Outbreaks in the European Union in 2008. p. 496. *In*, EFSA Journal, vol. 8.
606 European Food Safety Authority, Parma.
- 607 22. Farber, J. M., W. H. Ross, and J. Harwig. 1996. Health risk assessment of *Listeria*
608 *monocytogenes* in Canada. *Int. J. Food Microbiol.* 30:145-56.
- 609 23. Fondation de Technologie Laitière du Québec. 2002. Science et technologie du
610 lait. Transformation du lait. Presses internationales polytechnique, Montreal.
- 611 24. Garrido, V., I. García-Jalón, A. I. Vitas, and M. Sanaa. 2010. Listeriosis risk
612 assessment: Simulation modelling and "what if" scenarios applied to consumption of
613 ready-to-eat products in a Spanish population. *Food Control.* 21:231-239.

- 614 25. Gnanou Besse, N., N. Audinet, L. Barre, A. Cauquil, M. Cornu, and P. Colin.
615 2006. Effect of the inoculum size on *Listeria monocytogenes* growth in structured media.
616 *Int. J. Food Microbiol.* 110:43-51.
- 617 26. Graves, L. M., and B. Swaminathan. 2001. PulseNet standardized protocol for
618 subtyping *Listeria monocytogenes* by macrorestriction and pulsed-field gel
619 electrophoresis. *Int. J. Food Microbiol.* 65:55-62.
- 620 27. Havelaar, A. H., E. G. Evers, and M. J. Nauta. 2008. Challenges of quantitative
621 microbial risk assessment at EU level. *Trends Food Sc. Technol.* 19:S26-S33.
- 622 28. Iezzi, R., S. Francolino, and G. Mucchetti. 2011. Natural convective cooling of
623 cheese: Predictive model and validation of heat exchange simulation. *J. Food Eng.*
624 106:88-94.
- 625 29. International Commission on. Microbiological Specifications for Foods. 1996.
626 Microorganism in foods. Characteristics of Microbial pathogens. Blackie Academic &
627 Professional, London.
- 628 30. Jacquet, C., C. Saint-Clément, F. Brouille, B. Catimel, and J. Rocourt. 1998. La
629 listériose humaine en France en 1997, données du Centre National de Référence des
630 *Listeria*. *Bulletin épidémiologique hebdomadaire.* 33.
- 631 31. Jacquet, C., F. Brouille, C. Saint-Clément, B. Catimel, and J. Rocourt. 2000. La
632 listériose humaine en France en 1998 -- données du Centre national de référence des
633 *Listeria*. *Journal de Pédiatrie et de Puériculture.* 13:120-122.

- 634 32. McKay, M. D., R. J. Beckman, and W. J. Conover. 1979. A comparison of three
635 methods for selecting values of input variables in the analysis of output from a computer
636 code. *Technometrics*. 21:239-245.
- 637 33. McLauchlin, J. 1997. The identification of *Listeria* species. *Int. J. Food Microbiol.*
638 38:77-81.
- 639 34. Mellefont, L. A., T. A. McMeekin, and T. Ross. 2008. Effect of relative inoculum
640 concentration on *Listeria monocytogenes* growth in co-culture. *Int. J. Food Microbiol.*
641 121:157-168.
- 642 35. Meyer-Broseta, S., A. Diot, S. Bastian, J. Riviere, and O. Cerf. 2003. Estimation
643 of low bacterial concentration: *Listeria monocytogenes* in raw milk. *Int. J. Food*
644 *Microbiol.* 80:1-15.
- 645 36. Nauta, M. J., . 2001. A modular process risk model structure for quantitative
646 microbiological risk assessment and its application in an exposure assessment of *Bacillus*
647 *cereus* in a REPFED. p. 100. *In* National Institute of Public Health and the
648 Environment, Bilthoven.
- 649 37. Nightingale, K. K., Y. H. Schukken, C. R. Nightingale, E. D. Fortes, A. J. Ho, Z.
650 Her, Y. T. Grohn, P. L. McDonough, and M. Wiedmann. 2004. Ecology and
651 transmission of *Listeria monocytogenes* infecting ruminants and in the farm
652 environment. *Appl. Environ. Microbiol.* 70:4458-4467.

- 653 38. Pouillot, R., and M. B. Lubran. 2011. Predictive microbiology models vs.
654 modeling microbial growth within *Listeria monocytogenes* risk assessment: What
655 parameters matter and why. *Food Microbiol.* 28:720-726.
- 656 39. Rosenow, E. M., and E. H. Marth. 1987. Growth of *Listeria monocytogenes* in
657 skim, whole and chocolate milk and whipping cream during incubation at 4, 8, 13, 21
658 and 35°C. *J. Food Prot.* 50:452-459.
- 659 40. Saltelli, A. 2002. Making best use of model evaluations to compute sensitivity
660 indices. *Comput. Phys. Commun.* 145:280-297.
- 661 41. Saltelli, A. 2002. Sensitivity Analysis for Importance Assessment. *Risk Anal.*
662 22:579-590.
- 663 42. Saltelli, A., M. Ratto, T. Andres, F. Campolongo, J. Cariboni, D. Gatelli, M.
664 Saisana, and S. Tarantola. 2008. Global Sensitivity Analysis :The primer. Chichester,
665 West Sussex, England.
- 666 43. Saltelli, A., S. Tarantola, and F. Campolongo. 2000. Sensitivity Analysis as an
667 Ingredient of Modeling. *Stat. Sci.* 15.
- 668 44. Saltelli, A., S. Tarantola, F. Campolongo, and R. Marco. 2007. Sensitivity
669 Analysis in practice : A guide to assessing scientific models. Chichester, West Sussex,
670 England.

- 671 45. Schvartzman, M. S., A. Maffre, F. Tenenhaus-Aziza, M. Sanaa, F. Butler, and K.
672 Jordan. 2011. Modelling the fate of *Listeria monocytogenes* during manufacture and
673 ripening of smeared cheese made with pasteurised or raw milk. *Int. J. Food Microbiol.*
674 145:531-538.

- 675 46. Seeliger, H. P. R., and K. Höhne. 1979. Chapter II Serotyping of *Listeria*
676 *monocytogenes* and Related Species. p. 31-49. *In* T. Bergan, and J.R. Norris (ed.),
677 *Methods in Microbiology*, vol. Volume 13. Academic Press.

- 678 47. Vanholme, L., H. Imberechts, G. Ducoffre, and K. Dierick. 2009. Report of
679 zoonotic agents in Belgium in 2007. p. 164. *In* The Veterinary and Agrochemical
680 Research centre, Brussels.

- 681 48. Vose, D. 2000. Risk analysis A quantitative guide. John Wiley & Sons Inc,
682 Chichester.

- 683 49. Vose, D. 2005. ModelAssist Advanced for @Risk. *In* V. Consulting (ed.) Risk
684 Thinking Ltd, Gent.

- 685 50. Wiedmann, M., J. Czajka, N. Bsat, M. Bodis, M. C. Smith, T. J. Divers, and C. A.
686 Batt. 1994. Diagnosis and epidemiological association of *Listeria monocytogenes* strains
687 in two outbreaks of listerial encephalitis in small ruminants. . *J. Clin. Microbiol.* 32:991-
688 996.

- 689 51. Wiedmann, M., J. L. Bruce, R. Knorr, M. Bodis, E. M. Cole, C. I. McDowell, P.
690 L. McDonough, and C. A. Batt. 1996. Ribotype diversity of *Listeria monocytogenes*

691 strains associated with outbreaks of listeriosis in ruminants. *J. Clin. Microbiol.* 34:1086-
692 90.

693

694

List of tables

Table 1:	Characterization of the model inputs	33
Table 2:	Calculation details to assess the contamination of a serving of cheese	35
Table 3:	Identification of input factors for the sensitivity analysis and their respective ranges of variation	36
	* measured values	36
Table 4:	Anamnesis elements in relation to the carrier animal	37
Table 5:	Baseline results of the exposure assessment and the risk characterization modules	39
Table 6:	Estimates of the first order (S_i) and total effect (St_i) indices of the sensitivity analysis and their bootstrap confidence intervals (p5 and p95)	40
Table 7:	Results of the scenarios analysis (Concentration of <i>L. monocytogenes</i> in a cheese (log CFU/g))	41

710 **Table 1:** Characterization of the model inputs

Cheese making process		Parameter	Description	Values / Distributions	Units
0. Characterization of the milk production		N_{goat}	Number of goats	350	goats
		$N_{goat\ prod}$	Number of goats for the cheese production	$P(160;170;180)$	goats
		$N_{contaminated\ goat}$	Number of contaminated goats for the cheese production	1	goats
		$Q_{milk\ goat/day}$	Quantity of milk per goat per day	$P(2.5;3;3.5)$	litres/day
		$N_{milkmg/day}$	Number of milkings per day	2	times/day
		L_{cheese}	Numbers of litres per 1 Kg of cheese	$P(4.5;5.5)$	litres
		W_{cheese}	Weight of cheese	$P(95;100;105)$	g
		$N_{days\ prod}$	Number of days for cheese production per week	5	days
		$N_{week\ prod}$	Number of weeks of production with the contaminated milk	19	weeks
		$N_{servings/cheese}$	Number of servings per cheese	2	servings
1. Storage of the evening milk		$T_{start, tank\ evening}$	Initial temperature of milk collected in the evening	39.5	°C
		$T_{end, tank\ evening}$	Final temperature of milk collected in the evening	$P(9;10;12)$	°C
		$D_{tank\ evening}$	Duration of the evening milk storage overnight	$P(13;14;15)$	h
2. Storage of the morning milk		$T_{start, tank\ morning}$	Initial temperature of milk collected in the morning	39.5	°C
		$T_{end, tank\ morning}$	Final temperature of milk collected in the morning	$P(20;22;24)$	°C
		$D_{tank\ morning}$	Duration of the morning milk storage before mixing	1	h
3. Mixing		$T_{end, mix}$	Milk temperature after mixing	$P(20;22;24)$	°C
		D_{mix}	Duration of the step mixing of the morning and evening milk	1	h
4. Adjunction of starter		$T_{starter}$	Milk temperature at the step adjunction of starter	$P(20;22;24)$	°C
		$D_{starter}$	Duration of the step adjunction of starter	2	h
		$pH_{starter}$	pH at the end of the step adjunction of starter	6.3	pH units
5. Adjunction of rennet		T_{rennet}	Milk temperature at the adjunction of rennet	$P(20;22;24)$	°C
		D_{rennet}	Duration of the step adjunction of rennet	22	h
		pH_{rennet}	pH at the end of the step adjunction of rennet	4.41	pH units
6. Draining off curdles		$T_{curdles}$	Temperature at the step draining off curdles	$P(20;22;24)$	°C
		$D_{curdles}$	Duration of the step draining off curdles	0.5	h
		$T_{salting1}$	Temperature at the step Salting 1	$P(19;20;21)$	°C
7. Saltings 1 and 2		$D_{salting1}$	Duration of the step Salting 1	24	h
		$pH_{salting1}$	Final pH obtained after the step Salting 1	4.28	pH units
		$T_{salting2}$	Temperature at the step Salting 2	$P(14;16;18)$	°C
		$D_{salting2}$	Duration of the step Salting 2	48	h
		$pH_{salting2}$	Final pH obtained after the step Salting 2	4.42	pH units
8. Cooled storage		$T_{storage}$	Temperature of the cooled storage	$P(0;1;2)$	°C
		$D_{storage}$	Duration of the cooled storage	48	h

712

<i>L. monocytogenes</i> / matrices		Parameter	Description	Values / Distributions	Units	References
characteristics		T_{min}	Minimum temperature for growth (°C)	$N(-1.8;0.72)$	°C	
		T_{opt}	Optimal temperature for growth (°C)	$N(38.2;0.76)$	°C	
		T_{max}	Maximal temperature for growth (°C)	$N(43.3;1.2)$	°C	
<i>L. monocytogenes</i> characteristics		pH_{min}	Minimum pH for growth	$N(4.19;0.12)$	pH units	(7, 19, 29)
		pH_{opt}	Optimal pH for growth	7	pH units	
		pH_{max}	Maximum pH for growth	9.61	pH units	
		$a_{w\ min}$	Minimum a_w for growth	$N(0.922;0.009)$	a_w units	
		$a_{w\ opt}$	Optimal a_w for growth	0.997	a_w units	
		$a_{w\ max}$	Maximal a_w for growth	1	a_w units	
<i>Growth characteristics in milk</i>		$\mu_{opt,milk}$	Optimal growth rate in milk	$N(0.75; 0.13)$	h^{-1}	(8, 39)
		N_{max}	Maximum concentration in milk	7	log CFU/ml	
		pH_{milk}	pH of the milk	6.63	pH units	(measured)
		$a_{w\ milk}$	a_w of the milk	0.99	a_w units	(measured)
<i>Growth characteristics in cheese</i>		$\mu_{opt,cheese}$	Optimal growth rate in cheese	$NT(0.21;0.19;0.02;0.6)$	h^{-1}	(8, 39)
		N_{max}	Maximum concentration in cheese	7	log CFU/g	
		pH_{cheese}	pH of the cheese	4.28	pH units	(measured)
		$a_{w\ cheese}$	a_w of the cheese	0.977	a_w units	(measured)

713 $N(m; s)$, normal distribution with expected value m and standard deviation s .
714 $NT(m; s; a; b)$ normal distribution with expected value m and standard deviation s truncated on $[a; b]$.
715 $P(a; b, c)$ = Pert distribution with the minimum a , most likely b and maximum values c

716 **Table 2:** Calculation details to assess the contamination of a serving of cheese

Parameters	Description	Calculations	Units
Milk production			
$Q_{milk/milking}$	Quantity of milk per milking ($Q_{milk.morning}$ or $Q_{milk.evening}$)	$Q_{milk/milking} = Q_{milk/goat/day} / N_{milking/day}$	litres/milking
$N_{cheese/batch}$	Number of cheeses per batch	$N_{cheese/batch} = N_{goat prod} * Q_{milk/goat/day} / L_{cheese} * 1000 / W_{cheese}$	units
$N_{cheese/prod}$	Number of cheeses produced with the contaminated milk	$N_{cheese/prod} = N_{cheese/batch} * N_{days.prod} * N_{week.prod}$	units
$N_{cont.servings}$	Number of contaminated servings	$N_{cont.servings} = N_{cheese/prod} * N_{servings}$	servings
Storage of the evening milking (module 1)			
$C_{ini.conc}$	Concentration of <i>L. monocytogenes</i> in the milk from the right mammary gland of the shedder goat	$4.3.10^2$ (i.e. 2.63 log CFU/ml)	CFU/ml
$N_{milking}$	Number of <i>L. monocytogenes</i> from the infected goat per milking	$N_{milking} = C_{ini.conc} * 1000 * Q_{milk/milking} / 2$	CFU/milking
$C_{tank evening milk}$	Concentration of <i>L. monocytogenes</i> in a tank before storage over night of the evening milk	$C_{tank evening milk} = Pois(N_{milking} / (N_{goat prod} * Q_{milk/milking} * 1000))$	CFU/ml
$C_{tank night stor}$	Concentration of <i>L. monocytogenes</i> in a tank after storage over night of the evening milk	Dynamic predictive microbial model, equations 1 to 4 (table 1)	CFU/ml
Storage of the morning milking, mixing of milkings and adjunction of ferment and rennet (modules 2, 3, 4 and 5)			
$C_{tank morning milk}$	Concentration of <i>L. monocytogenes</i> in a tank before storage of the morning milk	$C_{tank morning milk} = Pois(N_{milking} / (N_{goat prod} * Q_{milk/milking} * 1000))$	CFU/ml
$C_{tank morning stor}$	Concentration of <i>L. monocytogenes</i> in a tank after storage of the morning milk	Dynamic predictive microbial model, equations 1 to 4 (table 1)	CFU/ml
$C_{after mix}$	Concentration of <i>L. monocytogenes</i> in a tank after mixing	$C_{after mix} = (C_{tank night stor} / 2) + (C_{tank morning stor} / 2)$	CFU/ml
$C_{ferment, rennet}$	Concentration in milk before draining off the curdles	Dynamic predictive microbial model, equations 1 to 4 (table 1)	CFU/ml
Draining off of curdles, storage and salting, cooled storage and wrapping (modules 6, 7 and 8)			
C_{cheese}	Concentration of <i>L. monocytogenes</i> per cheese before storage and salting	$C_{cheese} = (C_{ferment, rennet} * 1000 * L_{cheese} * (90/100)) / 1000$	CFU/g
N_{cheese}	Number of <i>L. monocytogenes</i> per cheese	$N_{cheese} = C_{cheese} * W_{cheese}$	CFU/cheese
$C_{serving}$	Number of <i>L. monocytogenes</i> per cheese at presentation to customers	Dynamic predictive microbial model, equations 1 to 4 (table 1)	CFU/g
$N_{serving}$	Number of <i>L. monocytogenes</i> per serving of cheese	$N_{serving} = C_{serving} * W_{cheese} / N_{servings/cheese}$	CFU/serving

717 *Pois*(λ)=Poisson distribution with the lambda value

718

719

720

722

Table 3: Identification of input factors for the sensitivity analysis and their respective ranges of variation

	Parameters	Description	Units	Value in the model	Ranges of variation
Cheese making process	$N_{\text{goat prod}}$	Number of goats for the cheese production	goats	$P(160; 170; 180)$	50-1000
	$N_{\text{contaminated.goat}}$	Number of contaminated goats	goats	1	1-50
	$N_{\text{mamgalnd.ex}}$	Number of excreting mammary glands	glands	1	1-2
	$T_{\text{end.tank.evening}}$	Final temperature of milk collected in the evening	°C	$P(9;10;12)$	5-14
	$D_{\text{tank.evening}}$	Duration of the evening milk storage overnight	h	$P(13;14;15)$	10-18
	$T_{\text{end.tank.morning}}$	Final temperature of milk collected in the morning	°C	$P(20;22;24)$	17-27
	$D_{\text{tank.morning}}$	Duration of the morning milk storage before mixing	h	1	1-8
	pH_{starter}	pH at the end of the step adjunction of starter	pH units	6.30 *	5.5-7.0
	D_{rennet}	Duration of the step adjunction of rennet	h	22	18-24
	pH_{rennet}	pH at the end of the step adjunction of rennet	pH units	4.41 *	4.0-5.0
	D_{Curdles}	Duration of the step draining off curdles	h	0.5	0.25-2.00
	T_{salting1}	Temperature at the step Salting 1	°C	$P(19;20;21)$	17-27
	D_{salting1}	Duration of the step Salting 1	h	24	12-72
	pH_{salting1}	Final pH obtained after the step Salting 1	pH units	4.28 *	4.00-5.00
	T_{salting2}	Temperature at the step Salting 2	°C	$P(14;16;18)$	10-22
	D_{salting2}	Duration of the step Salting 2	h	48	36-96
	pH_{salting2}	Final pH obtained after the step Salting 2	pH units	4.42	4.00-5.00
T_{storage}	Temperature of the cooled storage	°C	$P(0;1;2)$	-1-5	
D_{storage}	Duration of the cooled storage	h	48	24-96	
<i>L. monocytogenes</i> characteristics	N_0	Initial concentration of <i>L. monocytogenes</i>	CFU/ml	$4.3.10^2$	0.00-10000
	T_{min}	Minimum temperature for growth (°C)	°C	$N(-1.8;0.72)$	-5- -1
	T_{opt}	Optimal temperature for growth (°C)	°C	$N(38.2;0.76)$	35- 41
	T_{max}	Maximum temperature for growth (°C)	°C	$N(43.3;1.2)$	41- 45
	pH_{min}	Minimum pH for growth	pH units	$N(4.19;0.12)$	3.00-5.00
	pH_{opt}	Optimal pH for growth	pH units	7	6.00-8.00
	pH_{max}	Maximum pH for growth	pH units	9.61	8.0-10.0
	$a_w \text{ min}$	Minimum a_w for growth	a_w units	$N(0.922;0.009)$	0.850-0.960
	$a_w \text{ opt}$	Optimal a_w for growth	a_w units	0.997	0.98-0.995
	$a_w \text{ max}$	Maximum a_w for growth	a_w units	1	0.995-1
	$\mu_{\text{opt.milk}}$	Optimal growth rate in milk	h ⁻¹	$N(0.75;0.13)$	0.50-1.00
	pH_{milk}	pH of the milk	pH units	6.63	6.00-7.00
	$a_w \text{ milk}$	a_w of the milk	a_w units	0.99	0.990-1.000
	$\mu_{\text{opt.cheese}}$	Optimal growth rate in cheese	h ⁻¹	$NT(0.21;0.19;0.02;0.6)$	0.02-0.61
	pH_{cheese}	pH of the cheese	pH units	4.28	3.80-5.20
	$a_w \text{ cheese}$	a_w of the cheese	a_w units	0.977	0.960-0.990

725 $N(m; s)$, normal distribution with expected value m and standard deviation s .

726 $NT(m; s; a; b)$ normal distribution with expected value m and standard deviation s truncated on $[a; b]$.

727 $P(a; b; c)$ = Pert distribution with the minimum a , most likely b and maximum values c

728 * measured values

729

730 **Table 4:** Anamnesis elements in relation to the carrier animal

Date	Event	Remark / result
22 February 2004	birth of the shedder goat	
20 March 2005	Analyses of final products (goat cheeses made from raw milk) upon request of the FASFC. Results of analyses favourable (i.e. no <i>L. monocytogenes</i> found in the products)	no <i>L. monocytogenes</i> found in the products
In March 2005	Dropping of the shedder goat and start of the lactation process for this goat.	
11 July 2005	New analyses of final products (goat cheeses) upon request of the FASFC in an external laboratory. The herd is then blocked and the sale of cheese is prohibited by FASFC. The farmer himself performs the recall of products.	Positive results (i.e. <i>L. monocytogenes</i> isolated in the samples: presence in 25 g samples).
12 July 2005	Numbers of <i>L. monocytogenes</i> in different final products. Serotyping performed	<ul style="list-style-type: none"> ▪ fresh cheese not ripened: 4.3.10³ CFU/g ; ▪ goat cheese ripened: 6.5.10³ CFU/g ▪ goat cheese ripened and coated with charcoal: 5.1.10³ CFU/g Serotype 1/2a with a β -hemolysis.
15 July 2005 to 18 July 2005	Seeking out the excreting goat by analysing pools of 20 samples of milk from goats collected directly after the milking process.	Only 1 pool was positive with identification of only one clearly excreting goat in the herd.
19 July 2005	Transfer of the goat to the faculty of veterinary medicine (Liège University).	No clinical signs were observed in this animal after complete clinical examination.
End of July 2005	Re-start of the fabrication process with mandatory analyses imposed by the competent authority in order to perform a surveillance of <i>L. monocytogenes</i> contamination in the final products (5 samples on the 1st batch of the final products, then 1 sample each [for the next] 5 batches of final products – both ripened goat cheese and not ripened).	no <i>L. monocytogenes</i> found in the products (in 25-g of analytical samples)
14 September to 22 September 2005	Milk samples taken on the hospitalized goat in the two different parts of the mammary gland.	<ul style="list-style-type: none"> ▪ 4.3.10² CFU <i>L. monocytogenes</i>/ml for the right part. [The isolated strain will harbour the following internal lab reference: 05/180 D] ▪ Absence of <i>L. monocytogenes</i> in 25 ml for the left part of the mammary gland
4 October 2005	The isolated strain is sent to the National Reference Laboratory for Listeria (NRL) in Brussels (Scientific Institute of Public Health). Meanwhile, another strain (the one isolated from the cheese; analyses performed by another external accredited laboratory) was also sent to the National Reference Laboratory (so the NRL had two strains originating from this farm).	
11 October to 3 November 2005	Serotyping at the National Reference Laboratory, antibiogram and PFGE (Pulse Field Gel Electrophoresis) on one strain isolated in the milk, one strain isolated in the cheese and three strains of human origin (collected from human patients with	confirmation of serotype 1/2a, with a β -hemolysis

	listeriosis).	
September to December 2005	Request of surveillance of final products in the herd at a frequency of 1 analysis/15 days of production	no <i>L. monocytogenes</i> found in the products
From January 2006	Request of surveillance of final products in the herd at a frequency of 1 analysis/6 months of production (with the following parameters: <i>Listeria</i> , <i>Salmonella</i> , <i>E. Coli</i> and coagulase – positive <i>Staphylococci</i>).	no <i>L. monocytogenes</i> found in the products

731

732

733 **Table 5:** Baseline results of the exposure assessment and the risk characterization modules

734

Modules	Item	Acronym	Percentiles			Unit
			5 th	50 th	95 th	
Milking	Concentration in a tank before storage over night of the evening milk	$C_{\text{tank evening milk}}$	-5	0	0.47	log CFU/ml
Storage of the evening milk before mixing	Concentration in the tank after storage over night of the evening milk	$C_{\text{tank night stor}}$	-3.2	2.2	3.1	log CFU/ml
Adjunction of ferment and rennet	Concentration before draining off the curdles	$C_{\text{ferment,rennet}}$	-2.2	3.2	4.1	log CFU/ml
Draining off the curds	Number of <i>L. monocytogenes</i> per cheese	N_{cheese}	0.5	5.8	6.8	log CFU/cheese
Cooled storage and wrapping	Concentration of <i>L. monocytogenes</i> in a serving of cheese	C_{serving}	-1.5	3.8	4.8	log CFU/g
	Number of <i>L. monocytogenes</i> per serving of cheese	N_{serving}	0.2	5.5	6.5	log CFU/serving

735

736

737

Table 6: Estimates of the significant first order (S_i) and total effect (St_i) indices of the sensitivity analysis and their bootstrap confidence intervals (p5 and p95)

Parameters	Description	Ranges of variation	St_i	[p5	p95]	S_i	[p5	p9
$D_{salting1}$	Duration of the salting step 1	12-72	0,78	0,68	0,88	-0,14	-0,20	-0,
pH_{min}	Minimum pH for growth	3.00-5.00	0,40	0,30	0,50	-0,14	-0,19	-0,
μ_{opt_milk}	Optimal growth rate in milk	0,50-1,00	0,19	0,08	0,30	-0,20	-0,23	-0,
N_0	Initial concentration of <i>L. monocytogenes</i>	0.00-4.00	0,12	0,02	0,23	0,00	-0,03	0,0

743 **Table 7:** Results of the scenarios analysis (Concentration of *L. monocytogenes* in a
 744 cheese (log CFU/g))

Scenarios	Percentiles		
	5 th	50 th	95 th
Baseline results	-1.5	3.8	4.8
Scenario 1: Installation of a heat exchanger plate to obtain a temperature of 7 °C directly after milking and maintain a constant temperature during the overnight storage.	-2.9	2.3	2.8
Scenario 2: pH reduction of 0.5 units at the start of adjunction of ferment and rennet. This could be achieved, for example, by adjunction of food acid.	-1.7	3.6	4.6
Scenario 3: Increase efforts in the production by combining previous scenarios.	-3.1	2.0	2.6
Scenario 4: 2 shedder goats excreting each 2.6 log <i>L. monocytogenes</i> /ml in the right part of the mammary gland.	-1.0	4.2	5.1

745

1 List of figures

Figure 1:	Presentation of the exposure assessment model	43
Figure 2:	Evolution of <i>L. monocytogenes</i> concentration in function (a) of temperature during the storage of the evening milk and (b) pH after the adjunction of rennet to milk steps	44

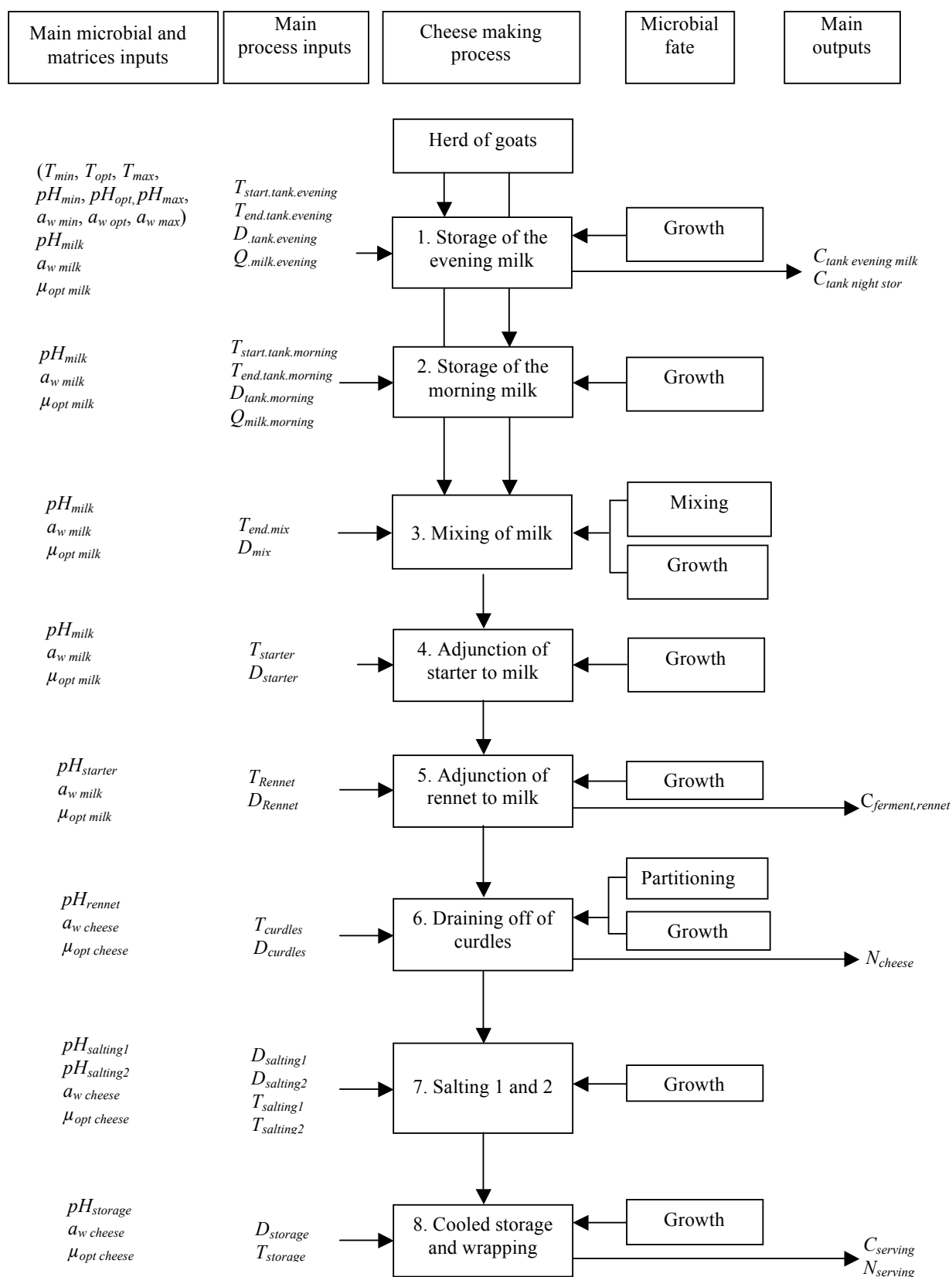


Figure 1: Presentation of the exposure assessment model

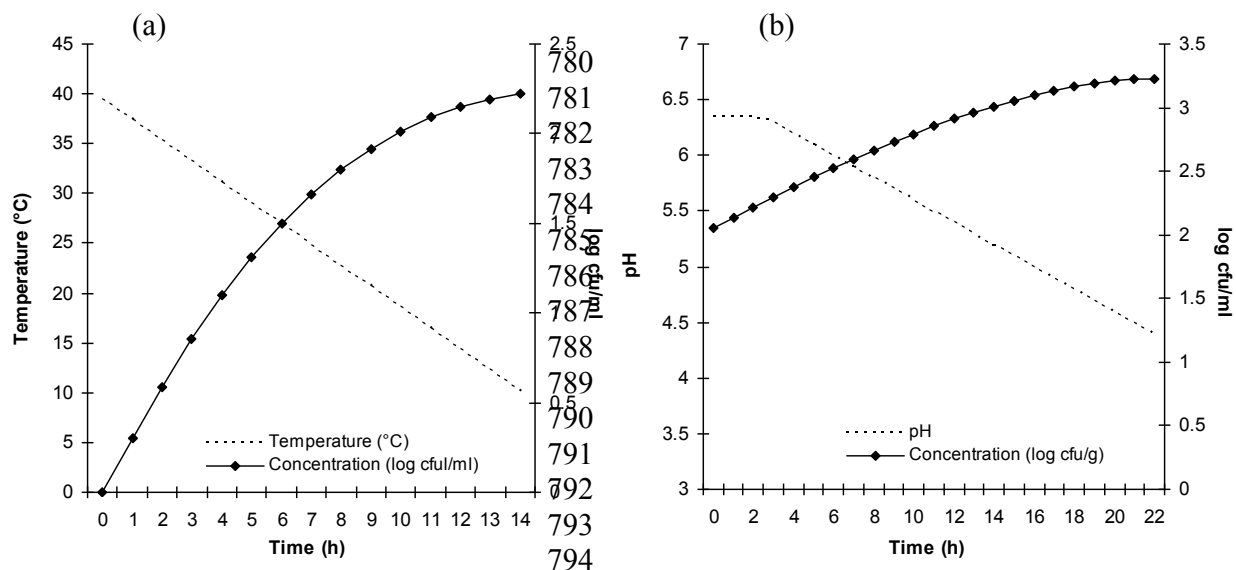


Figure 2: Evolution of *L. monocytogenes* concentration in function (a) of temperature during the storage of the evening milk in the tank and (b) pH after the adjunction of rennet to milk steps